

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).

3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).

4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached marked-up copy of the "Raw Sequence Listing."

5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).

6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).

7. Other: _____

Applicant must provide:

An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"

An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification

A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123
For CRF submission help, call (703) 308-4212
For PatentIn software help, call (703) 308-6856

Please return a copy of this notice with your response.

#8



1638

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/643,755B

DATE: 01/23/2002 FEB 06 2002
TIME: 17:11:35

TECH CENTER 1600/2900

Input Set : A:\Sequence
Output Set: N:\CRF3\01232002\I643755B.raw

4 <110> APPLICANT: van Rooijen, Gijs
 5 Keon, Richard Glenn
 6 Boothe, Joseph
 7 Shen, Yin
 9 <120> TITLE OF INVENTION: Commercial Production of Chymosin in Plants
 11 <130> FILE REFERENCE: 9369-153
 13 <140> CURRENT APPLICATION NUMBER: 09/643,755B
 14 <141> CURRENT FILING DATE: 2000-08-23
 16 <160> NUMBER OF SEQ ID NOS: 4
 18 <170> SOFTWARE: PatentIn Ver. 2.0
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 1173
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Bovine
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (1)..(1173)
 29 <400> SEQUENCE: 1
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 32 1 5 10 15
 34 caa tac ttc gtt gct act cac gct gct gag atc acc acc cgcc att cct 96
 35 Gln Tyr Phe Val Ala Val Thr His Ala Ala Glu Ile Thr Arg Ile Pro
 36 20 25 30
 38 ctc tac aaa ggt aag tct ctc cgt aag gcg ctg aag gaa cat gga ctt 144
 39 Leu Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu
 40 35 40 45
 42 cta gaa gac ttc ttg cag aaa caa cag tat ggc atc agc agc aag tac 192
 43 Leu Glu Asp Phe Leu Gln Lys Gln Gln Tyr Gly Ile Ser Ser Lys Tyr
 44 50 55 60
 46 tcc ggc ttc ggt gaa gtt gct agc gtg cca ctt acc aac tac ctt gat 240
 47 Ser Gly Phe Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp
 48 65 70 75 80
 50 agt caa tac ttt ggg aag atc tac ctc gga acc ccg cct caa gag ttc 288
 51 Ser Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe
 52 85 90 95
 54 acc gtt ctc ttt gat act ggt tcc tct gac ttc tgg gtt ccc tct atc 336
 55 Thr Val Leu Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile
 56 100 105 110
 58 tac tgc aag agc aat gcc tgc aag aac cac caa aga ttc gat ccg aga 384
 59 Tyr Cys Lys Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg
 60 115 120 125
 62 aag tcg tcc acc ttc cag aac tta ggc aaa ccc ttg tct ata cac tac 432

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63	Lys Ser Ser Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr			
64	130	135	140	
66	ggt aca ggt agc atg caa gga atc tta ggc tat gat acc gtc act gtc	480		
67	Gly Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val			
68	145	150	155	160
70	tcc aac att gtg gac att caa cag aca gta gga ctt agc acc caa gaa	528		
71	Ser Asn Ile Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu			
72	165	170	175	
74	cca ggt gat gtc ttc acc tat gca gaa ttc gat ggc atc ctt ggt atg	576		
75	Pro Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met			
76	180	185	190	
78	gca tac cca tcg ctc gcg tca gag tac tcg ata cct gtg ttt gac aac	624		
79	Ala Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn			
80	195	200	205	
82	atg atg aac cga cac cta gta gct caa gac ttg ttc tcg gtt tac atg	672		
83	Met Met Asn Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met			
84	210	215	220	
86	gac agg aat ggc cag gag agc atg ctc acg ctt gga gct att gat cca	720		
87	Asp Arg Asn Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro			
88	225	230	235	240
90	tcc tac tac aca gga tct ctt cac tgg gtt cca gtc act gtg cag cag	768		
91	Ser Tyr Tyr Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln			
92	245	250	255	
94	tac tgg caa ttc act gtg gac agt gtc acc atc agc ggt gtg gtt gtt	816		
95	Tyr Trp Gln Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val			
96	260	265	270	
98	gca tgt gaa ggt gga tgt caa gct atc ttg gat acc ggt acg tcc aag	864		
99	Ala Cys Glu Gly Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys			
100	275	280	285	
102	ctg gtc gga cct agc agc gac att ctc aac att cag caa gct att gga	912		
103	Leu Val Gly Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly			
104	290	295	300	
106	gcc aca cag aac cag tac ggt gag ttt gac ata gat tgc gac aac ctt	960		
107	Ala Thr Gln Asn Gln Tyr Gly Glu Phe Asp Ile Asp Cys Asp Asn Leu			
108	305	310	315	320
110	agc tac atg cct aca gtt gtc ttt gag atc aac ggc aag atg tac cca	1008		
111	Ser Tyr Met Pro Thr Val Val Phe Glu Ile Asn Gly Lys Met Tyr Pro			
112	325	330	335	
114	ctg acc ccc tcc gcc tat acc agc cag gat caa ggg ttc tgc acc agt	1056		
115	Leu Thr Pro Ser Ala Tyr Thr Ser Gln Asp Gln Gly Phe Cys Thr Ser			
116	340	345	350	
118	gga ttc cag agt gag aac cat tcc cag aaa tgg atc ttg gga gat gtg	1104		
119	Gly Phe Gln Ser Glu Asn His Ser Gln Lys Trp Ile Leu Gly Asp Val			
120	355	360	365	
122	ttc att cgt gag tac tac agc gtc ttt gac agg gcc aac aac ctc gtt	1152		
123	Phe Ile Arg Glu Tyr Tyr Ser Val Phe Asp Arg Ala Asn Asn Leu Val			
124	370	375	380	
126	ggg cta gct aaa gca atc tga	1173		
127	Gly Leu Ala Lys Ala Ile			

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128 385 390
 131 <210> SEQ ID NO: 2
 132 <211> LENGTH: 390
 133 <212> TYPE: PRT
 134 <213> ORGANISM: Bovine
 136 <400> SEQUENCE: 2
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 140 Gln Tyr Phe Val Ala Val Thr His Ala Ala Glu Ile Thr Arg Ile Pro
 141 20 25 30
 143 Leu Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu
 144 35 40 45
 146 Leu Glu Asp Phe Leu Gln Lys Gln Gln Tyr Gly Ile Ser Ser Lys Tyr
 147 50 55 60
 149 Ser Gly Phe Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp
 150 65 70 75 80
 152 Ser Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe
 153 85 90 95
 155 Thr Val Leu Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile
 156 100 105 110
 158 Tyr Cys Lys Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg
 159 115 120 125
 161 Lys Ser Ser Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr
 162 130 135 140
 164 Gly Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val
 165 145 150 155 160
 167 Ser Asn Ile Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu
 168 165 170 175
 170 Pro Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met
 171 180 185 190
 173 Ala Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn
 174 195 200 205
 176 Met Met Asn Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met
 177 210 215 220
 179 Asp Arg Asn Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro
 180 225 230 235 240
 182 Ser Tyr Tyr Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln
 183 245 250 255
 185 Tyr Trp Gln Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val
 186 260 265 270
 188 Ala Cys Glu Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys
 189 275 280 285
 191 Leu Val Gly Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly
 192 290 295 300
 194 Ala Thr Gln Asn Gln Tyr Gly Glu Phe Asp Ile Asp Cys Asp Asn Leu
 195 305 310 315 320
 197 Ser Tyr Met Pro Thr Val Val Phe Glu Ile Asn Gly Lys Met Tyr Pro
 198 325 330 335
 200 Leu Thr Pro Ser Ala Tyr Thr Ser Gln Asp Gln Gly Phe Cys Thr Ser

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**Input Set : A:\Sequence
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201 340 345 350
 203 Gly Phe Gln Ser Glu Asn His Ser Gln Lys Trp Ile Leu Gly Asp Val
 204 355 360 365
 206 Phe Ile Arg Glu Tyr Tyr Ser Val Phe Asp Arg Ala Asn Asn Leu Val
 207 370 375 380
 209 Gly Leu Ala Lys Ala Ile
 210 385 390
 213 <210> SEQ ID NO: 3
 214 <211> LENGTH: 3957
 215 <212> TYPE: DNA
 216 <213> ORGANISM: Artificial Sequence
 218 <220> FEATURE:
 219 <221> NAME/KEY: CDS
 220 <222> LOCATION: (1554)..(2726)
 222 <220> FEATURE:
 223 <223> OTHER INFORMATION: Description of Artificial Sequence: Phaseolin promoter- pre-
 pro-
 224 chymosin-phaseolin terminator
 226 <400> SEQUENCE: 3
 227 ctgcaggaat tcattgtact cccagtatca ttatagtgaa agttttggct ctctcgccgg 60
 229 tggttttta cctctattta aagggtttt ccacctaaaa attctggtat cattctcact 120
 231 ttacttggta cttaatttc tcataatctt tggttgaat tatacgcctt ccgcacacga 180
 233 tatccctaca aatttattat ttgttaaaca ttttcaaac gcataaaattt ttatgaagtc 240
 235 ccgtctatct ttaatgttagt ctaacatttt catattgaaa tatataattt acttaatttt 300
 237 agcgttggta gaaagcataa agatttattc ttattcttct tcatataaat gtttaatata 360
 239 caatataaaac aaattcttta cttaagaag gatttcccat tttatattt aaaaatataat 420
 241 ttatcaaata ttttcaacc acgttaatct cataataata agttgtttca aaagtaataa 480
 243 aatttaactc cataattttt ttattcgact gatcttaaag caacacccag tgacacaact 540
 245 agccatttt ttctttgaat aaaaaaatcc aattatcatt gtatttttt tatacaatga 600
 247 aaatttcacc aaacaatcat ttgttgtatt tctgaagcaa gtcatgttat gcaaaattct 660
 249 ataattccca tttgacacta cggaaagtaac tgaagatctg cttttacatg cgagacacat 720
 251 cttctaaagt aattttataa atagttacta tattcaagat ttcatataatc aaatactcaa 780
 253 tattacttct aaaaaattaa ttagatataa tttaaatattt acttttttaa ttttaagttt 840
 255 aatttttgaa tttgtgacta ttgattttt attctactat gtttaatttg tttttagat 900
 257 agtttaaagt aatataaagt aatgttagtag agtgttagag tgttacccta aaccataaaac 960
 259 tataacattt atggtggact aattttcata tatttcttta tgcttttacc ttttcttgtt 1020
 261 atgttaagtcc gtaactagaa ttacagtggg ttgccatggc actctgttgt cttttggttc 1080
 263 atgcattgggt cttgcgcaag aaaaagacaa agaacaaga aaaaagacaa aacagagaga 1140
 265 caaaacgcaa tcacacaacc aactcaaatt agtcaactggc tgatcaagat cgccgcgtcc 1200
 267 atgtatgtct aatgccccatg caaagcaaca cgtgcttaac atgcacttta aatggctcac 1260
 269 ccatctcaac ccacacacaa acacattgcc tttttcttca tcatcaccac aaccacctgt 1320
 271 atatattcat tctttccgc cacctcaatt tcttcacttc aacacacgtc aacctgcata 1380
 273 tgcgtgtcat cccatgccccaa aatctccatg catgttccaa ccaccttctc tcttatataa 1440
 275 tacctataaaa tacctctaat atcactcaact tctttcatca tccatccatc cagagtacta 1500
 277 ctactctact actataatac ccacaacccaa ctcattatca atactactct act atg 1556
 278 Met
 279 1
 281 aac ttc ctt aag tct ttc cct ttc tac gct ttc ctt tgt ttc ggt caa 1604
 282 Asn Phe Leu Lys Ser Phe Pro Phe Tyr Ala Phe Leu Cys Phe Gly Gln
 283 5 10 15

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Output Set: N:\CRF3\01232002\I643755B.raw

285 tac ttc gtt gct gtt act cac gct gct gag atc acc cgc att cct ctc	1652
286 Tyr Phe Val Ala Val Thr His Ala Ala Glu Ile Thr Arg Ile Pro Leu	
287 20 25 30	
289 tac aaa ggt aag tct ctc cgt aag gcg ctg aag gaa cat gga ctt cta	1700
290 Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu Leu	
291 35 40 45	
293 gaa gac ttc ttg cag aaa caa cag tat ggc atc agc agc aag tac tcc	1748
294 Glu Asp Phe Leu Gln Lys Gln Tyr Gly Ile Ser Ser Lys Tyr Ser	
295 50 55 60 65	
297 ggc ttc ggt gaa gtt gct agc gtg cca ctt acc aac tac ctt gat agt	1796
298 Gly Phe Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp Ser	
299 70 75 80	
301 caa tac ttt ggg aag atc tac ctc gga acc ccg cct caa gag ttc acc	1844
302 Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe Thr	
303 85 90 95	
305 gtt ctc ttt gat act ggt tcc tct gac ttc tgg gtt ccc tct atc tac	1892
306 Val Leu Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile Tyr	
307 100 105 110	
309 tgc aag agc aat gcc tgc aag aac cac caa aga ttc gat ccg aga aag	1940
310 Cys Lys Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg Lys	
311 115 120 125	
313 tcg tcc acc ttc cag aac tta ggc aaa ccc ttg tct ata cac tac ggt	1988
314 Ser Ser Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr Gly	
315 130 135 140 145	
317 aca ggt agc atg caa gga atc tta ggc tat gat acc gtc act gtc tcc	2036
318 Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val Ser	
319 150 155 160	
321 aac att gtg gac att caa cag aca gta gga ctt agc acc caa gaa cca	2084
322 Asn Ile Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu Pro	
323 165 170 175	
325 ggt gat gtc ttc acc tat gca gaa ttc gat ggc atc ctt ggt atg gca	2132
326 Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met Ala	
327 180 185 190	
329 tac cca tcg ctc gcg tca gag tac tcg ata cct gtg ttt gac aac atg	2180
330 Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn Met	
331 195 200 205	
333 atg aac cga cac cta gta gct caa gac ttg ttc tcg gtt tac atg gac	2228
334 Met Asn Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met Asp	
335 210 215 220 225	
337 agg aat ggc cag gag agc atg ctc acg ctt gga gct att gat cca tcc	2276
338 Arg Asn Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro Ser	
339 230 235 240	
341 tac tac aca gga tct ctt cac tgg gtt cca gtc act gtg cag cag tac	2324
342 Tyr Tyr Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln Tyr	
343 245 250 255	
345 tgg caa ttc act gtg gac agt gtc acc atc agc ggt gtg gtt gtc gca	2372
346 Trp Gln Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val Ala	
347 260 265 270	
349 tgt gaa ggt gga tgt caa gct atc ttg gat acc ggt acg tcc aag ctg	2420

VERIFICATION SUMMARY

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